AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A method for the fermentative production of ~~at least one sulfur-containing fine chemical~~ L-methionine, which comprises the following steps:

a) ~~fermentation~~ fermenting in a medium cells of a coryneform ~~bacteria culture~~ bacterium for producing ~~the desired sulfur-containing fine chemical~~ L-methionine, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with methylenetetrahydrofolate reductase (metF) activity, wherein said heterologous nucleotide sequence comprises a nucleotide sequence encoding a metF protein having an amino acid sequence as set forth in SEQ ID NO: 2 or comprises a nucleotide sequence encoding a metF protein having an amino acid sequence with 95% homology or more to the sequence as set forth in SEQ ID NO: 2;

b) ~~concentration of the sulfur-containing fine chemical~~ concentrating L-methionine in the medium or in the bacterial cells, and

c) ~~isolation of the sulfur-containing~~ fine chemical isolating L-methionine.

2-4. (Cancelled).

5. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the metF-encoding sequence comprises a coding sequence ~~according to~~ as set forth in SEQ ID NO:1~~, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39~~, 41, 43, 45, 47, 49, 51 and 53 or a nucleotide sequence homologous thereto which codes for a protein with metF activity~~.

6. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the metF-encoding sequence codes for a protein with metF activity, said protein comprising an amino acid sequence ~~according to~~ as set forth in SEQ ID NO:2~~, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54 or an amino acid sequence homologous thereto which represents a protein with metF activity~~.

7. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the coding metF sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Currently amended) ~~A~~ The method as claimed in claim 7, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metF sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metF sequence has been integrated into the bacteria chromosome is used.

9. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the coding metF sequence is overexpressed.

10. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of ~~the desired sulfur-containing fine chemical~~ L-methionine has been ~~amplified or mutated~~ overexpressed ~~such that its activity is not influenced by metabolic metabolites~~.

11. (Cancelled).

12. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein coryneform bacteria are fermented in which, at the same time, ~~at least one of the genes selected from among~~

~~a) the~~ a lysC gene, which encodes an aspartate kinase,

~~b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,~~

~~c) the 3-phosphoglycerate kinase-encoding gene pgk,~~

~~d) the pyruvate carboxylase-encoding gene pyc,~~

~~e) the triose phosphate isomerase-encoding gene tpi,~~

~~f) the homoserine O-acetyltransferase-encoding gene metA,~~

~~g) the cystathionine gamma-synthase-encoding gene metB,~~

~~h) the cystathionine gamma-lyase-encoding gene metC,~~

~~i) the serine hydroxymethyltransferase-encoding gene glyA,~~

~~j) the O-acetylhomoserine sulfhydrylase-encoding gene metY,~~

~~k) the vitamin B12-dependent methionine synthase-encoding gene metH,~~

~~l) the phophoserine aminotransferase-encoding gene serC,~~

~~m) the phosphoserine phosphatase-encoding gene serB,~~

~~n) the serine acetyltransferase-encoding gene cysE, and~~

~~o) the hom gene, which encodes a homoserine dehydrogenase,~~

is overexpressed ~~or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins~~.

13. (Cancelled).

14. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein ~~microorganisms~~ the coryneform bacterium is of the species ~~Corynebacterium glutamicum are used~~ *Corynebacterium glutamicum*.

15-16. (Cancelled).

17. (New) A method for the production of L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform bacterium for producing of L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with with methylenetetrahydrofolate reductase (metF) activity, wherein the heterologous nucleotide sequence comprises a nucleotide sequence having 95% identity or more to the sequence as set forth in SEQ ID NO: 1;

b) concentrating L-methionine in the medium or in the bacterial cells; and

c) isolating L-methionine.

18. (New) The method of claim 17, wherein the coding metF sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

19. (New) The method of claim 17, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metF sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metF sequence has been integrated into the bacteria chromosome is used.

20. (New) The method of claim 17, wherein the coding metF sequence is overexpressed.

21. (New) The method of claim 17, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been overexpressed.

22. (New) The method of claim 17, wherein the coryneform bacterium is of the species *Corynebacterium glutamicum*.